

IN THE UNITED STATES PATENT AND TRADEMARK OFFICE

Examiner : Not yet assigned
Group : Not yet assigned
Applicants : Jens Kossmann et al.
Serial No. : Not yet assigned
Filed : Concurrently herewith
For : NUCLEIC ACID MOLECULES CODING FOR
DEBRANCHING ENZYMES FROM MAIZE

New York, New York
May 8, 2001

Hon. Commissioner for Patents
Washington, D.C. 20231

STATEMENTS IN SUPPORT OF AMENDMENTS TO
SEQUENCE LISTING UNDER 37 C.F.R. § 1.825(a)
AND IN SUPPORT OF COMPUTER READABLE
FORM SUBMISSION UNDER 37 C.F.R. § 1.821(e)

Sir:

In accordance with 37 C.F.R. § 1.825(a), I hereby state that the paper copy of the Sequence Listing enclosed herewith does not include new matter and is supported by the application as originally filed.

I also hereby state, in accordance with 37 C.F.R. § 1.821(e), that the content of the Computer Readable Form copy of the Sequence Listing submitted with the September 4, 1998 Preliminary Amendment in United States application no.

09/148,680 and the above-mentioned paper copy of the substitute Sequence Listing is the same.

Respectfully submitted,



James F. Haley, Jr. (Reg. No. 27,794)

Elinor K. Shin (Reg. No. 43,117)

Attorneys for Applicants

c/o FISH & NEAVE

1251 Avenue of the Americas

New York, New York 10020

Tel.: (212) 596-9000

Fax.: (212) 596-9090

SEQUENCE LISTING

(1) GENERAL INFORMATION:

(i) APPLICANT:

- (A) NAME: PlantTec Biotechnologie GmbH Forschung & Entwicklung
- (B) STREET: Hermannswerder 14
- (C) CITY: Potsdam
- (E) COUNTRY: Germany
- (F) POSTAL CODE: 14473

(ii) TITLE OF THE INVENTION: Nucleic acid molecules coding for debranching enzymes from maize

(iii) NUMBER OF SEQUENCES: 4

(iv) COMPUTER-READABLE VERSION:

- (A) DATA CARRIER: Floppy disk
- (B) COMPUTER: IBM PC compatible
- (C) OPERATING SYSTEM: PC-DOS/MS-DOS
- (D) SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPA)

(2) INFORMATION FOR SEQ ID NO: 1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1993 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Zea mays
- (F) TISSUE TYPE: Blattgewebe

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LOCATION: 1..1675

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 1:

| | |
|---|-----|
| GGC ACG AGG TCA AAA CTC CCT CCA GGG TCA GAT TTG CAA CAA GCT GCA | 48 |
| Gly Thr Arg Ser Lys Leu Pro Pro Gly Ser Asp Leu Gln Gln Ala Ala | |
| 1 5 10 15 | |
| ATT GTG GCT ATT CAG GAA GAG GAC CCT TAT AAT TGG GGG TAT AAC CCT | 96 |
| Ile Val Ala Ile Gln Glu Glu Asp Pro Tyr Asn Trp Gly Tyr Asn Pro | |
| 20 25 30 | |
| GTG GTT TGG GGC GTT CCA AAA GGA AGC TAT GCA AGT AAC CCA GAT GGT | 144 |
| Val Val Trp Gly Val Pro Lys Gly Ser Tyr Ala Ser Asn Pro Asp Gly | |
| 35 40 45 | |

| | |
|---|-----|
| CCA AGT CGT ATC ATT GAG TAC CGG CTG ATG GTG CAG GCC TTG AAT CGC | 192 |
| Pro Ser Arg Ile Ile Glu Tyr Arg Leu Met Val Gln Ala Leu Asn Arg | |
| 50 55 60 | |
| TTA GGT CTT CGA GTT GTC ATG GAT GTT GTA TAC AAT CAT CTA TAC TCA | 240 |
| Leu Gly Leu Arg Val Val Met Asp Val Val Tyr Asn His Leu Tyr Ser | |
| 65 70 75 80 | |
| AGT GGC CCT TTT GCC ATC ACT TCC GTG CTT GAC AAG ATT GTA CCT GGA | 288 |
| Ser Gly Pro Phe Ala Ile Thr Ser Val Leu Asp Lys Ile Val Pro Gly | |
| 85 90 95 | |
| TAC TAC CTC AGA AGG GAC TCT AAT GGT CAG ACT GAG AAC AGC GCG GCT | 336 |
| Tyr Tyr Leu Arg Arg Asp Ser Asn Gly Gln Thr Glu Asn Ser Ala Ala | |
| 100 105 110 | |
| GTG AAC AAT ACA GCA AGT GAG CAT TTC ATG GTT GAT AGA TTA ATC GTG | 384 |
| Val Asn Asn Thr Ala Ser Glu His Phe Met Val Asp Arg Leu Ile Val | |
| 115 120 125 | |
| GAT GAC CTT CTG AAT TGG GCA GTA AAT TAC AAA GTT GAC GGG TTC AGA | 432 |
| Asp Asp Leu Leu Asn Trp Ala Val Asn Tyr Lys Val Asp Gly Phe Arg | |
| 130 135 140 | |
| TTT GAT CTA ATG GGA CAT ATC ATG AAA AAG ACA ATG ATT AGA GCA AAA | 480 |
| Phe Asp Leu Met Gly His Ile Met Lys Lys Thr Met Ile Arg Ala Lys | |
| 145 150 155 160 | |
| TCG GCT CTT CAA AGC CTT ACA ATT GAT GAA CAT GGA GTA GAT GGT TCA | 528 |
| Ser Ala Leu Gln Ser Leu Thr Ile Asp Glu His Gly Val Asp Gly Ser | |
| 165 170 175 | |
| AAG ATA TAC TTG TAT GGT GAA GGA TGG AAC TTC GGT GAA GTT GCG GAA | 576 |
| Lys Ile Tyr Leu Tyr Gly Glu Gly Trp Asn Phe Gly Glu Val Ala Glu | |
| 180 185 190 | |
| AAT CAA CGT GGG ATA AAT GGA TCC CAG CTA AAT ATG AGT GGC ACT GGG | 624 |
| Asn Gln Arg Gly Ile Asn Gly Ser Gln Leu Asn Met Ser Gly Thr Gly | |
| 195 200 205 | |
| ATT GGT AGT TTC AAC GAT AGA ATC CGT GAT GCT ATA AAT GGT GGC AGT | 672 |
| Ile Gly Ser Phe Asn Asp Arg Ile Arg Asp Ala Ile Asn Gly Gly Ser | |
| 210 215 220 | |
| CCG TTT GGG AAT CCA CTG CAA CAA GGT TTC TCT ACT GGA TTG TTC TTA | 720 |
| Pro Phe Gly Asn Pro Leu Gln Gln Gly Phe Ser Thr Gly Leu Phe Leu | |
| 225 230 235 240 | |
| GAG CCA AAT GGA TTT TAT CAG GGC AAT GAA ACA GAG ACA AGG CTC ACG | 768 |
| Glu Pro Asn Gly Phe Tyr Gln Gly Asn Glu Thr Glu Thr Arg Leu Thr | |
| 245 250 255 | |
| CTT GCT ACA TAC GCT GAC CAT ATA CAG ATT GGA TTA GCT GGC AAT TTG | 816 |
| Leu Ala Thr Tyr Ala Asp His Ile Gln Ile Gly Leu Ala Gly Asn Leu | |
| 260 265 270 | |
| AAG GAC TAT GTA GTT ATA TCT CAT ACT GGA GAA GCT AGA AAA GGA TCT | 864 |
| Lys Asp Tyr Val Val Ile Ser His Thr Gly Glu Ala Arg Lys Gly Ser | |
| 275 280 285 | |

| | |
|---|------|
| GAA ATT CGC ACC TTC GAT GGC TCA CCA GTT GGC TAT GCT TCA TCC CCT | 912 |
| Glu Ile Arg Thr Phe Asp Gly Ser Pro Val Gly Tyr Ala Ser Ser Pro | |
| 290 295 300 | |
| ATA GAA ACA ATA AAC TAC GCC TCT GCT CAT GAC AAT GAA ACA CTA TTT | 960 |
| Ile Glu Thr Ile Asn Tyr Ala Ser Ala His Asp Asn Glu Thr Leu Phe | |
| 305 310 315 320 | |
| GAT ATT ATT AGT CTA AAG ACT CCG ATG GAC CTC TCA ATT GAC GAG CGA | 1008 |
| Asp Ile Ile Ser Leu Lys Thr Pro Met Asp Leu Ser Ile Asp Glu Arg | |
| 325 330 335 | |
| TGC AGG ATA AAT CAT TTG TCC ACA AGC ATG ATT GCA TTA TCC CAG CGA | 1056 |
| Cys Arg Ile Asn His Leu Ser Thr Ser Met Ile Ala Leu Ser Gln Gly | |
| 340 345 350 | |
| ATA CCA TTT TTT CAT GCT GGT GAT GAG ATA CTA CGA TCT AAG TCG CTT | 1104 |
| Ile Pro Phe Phe His Ala Gly Asp Glu Ile Leu Arg Ser Lys Ser Leu | |
| 355 360 365 | |
| GAT CGA GAT TCA TAT GAC TCT GGT GAT TGG TTT AAC AAG ATT GAT TTT | 1152 |
| Asp Arg Asp Ser Tyr Asp Ser Gly Asp Trp Phe Asn Lys Ile Asp Phe | |
| 370 375 380 | |
| ACC TAT GAA ACA AAC AAT TGG GGT GTT GGG CTT CCA CCA AGA GAA AAG | 1200 |
| Thr Tyr Glu Thr Asn Asn Trp Gly Val Gly Leu Pro Pro Arg Glu Lys | |
| 385 390 395 400 | |
| AAC GAA GGG AGC TGG CCT TTG ATG AAG CCA AGA TTG GAG AAC CCG TCG | 1248 |
| Asn Glu Gly Ser Trp Pro Leu Met Lys Pro Arg Leu Glu Asn Pro Ser | |
| 405 410 415 | |
| TTC AAA CCT GCA AAA CAT GAC ATT ATT GCT GCC TTA GAC AAA TTT ATT | 1296 |
| Phe Lys Pro Ala Lys His Asp Ile Ile Ala Ala Leu Asp Lys Phe Ile | |
| 420 425 430 | |
| GAT ATC CTC AAG ATC AGA TAC TCA TCA CCT CTC TTT CGC CTA ACT ACA | 1344 |
| Asp Ile Leu Lys Ile Arg Tyr Ser Ser Pro Leu Phe Arg Leu Thr Thr | |
| 435 440 445 | |
| GCA AGT GAT ATT GTG CAA AGG GTT CAC TTT CAC AAC ACA GGG CCC TCC | 1392 |
| Ala Ser Asp Ile Val Gln Arg Val His Phe His Asn Thr Gly Pro Ser | |
| 450 455 460 | |
| TTG GTT CCA GGA GTT ATT GTC ATG AGC ATC GAA GAT GCA CGA AAT GAT | 1440 |
| Leu Val Pro Gly Val Ile Val Met Ser Ile Glu Asp Ala Arg Asn Asp | |
| 465 470 475 480 | |
| AGG CAT GAT ATG GCC CAG ATA GAT GAA ACA TTC TCT TGT GTC GTT ACA | 1488 |
| Arg His Asp Met Ala Gln Ile Asp Glu Thr Phe Ser Cys Val Val Thr | |
| 485 490 495 | |
| GTC TTC AAT GTA TGT CCG TAC GAA GTG TCT ATA GAA ATC CCT GAT CTT | 1536 |
| Val Phe Asn Val Cys Pro Tyr Glu Val Ser Ile Glu Ile Pro Asp Leu | |
| 500 505 510 | |
| GCA TCA CTG CGG CTT CAG TTG CAT CCA GTG CAG GTG AAT TCA TCG GAT | 1584 |
| Ala Ser Leu Arg Leu Gln Leu His Pro Val Gln Val Asn Ser Ser Asp | |
| 515 520 525 | |

| | |
|---|------|
| GCG TTA GCC AGG CAG TCT GCG TAC GAC ACC GCC ACA GGT CGA TTC ACC | 1632 |
| Ala Leu Ala Arg Gln Ser Ala Tyr Asp Thr Ala Thr Gly Arg Phe Thr | |
| 530 535 540 | |
| | |
| GTG CCG AAA AGG ACA GCA GCA GTG TTC GTG GAA CCC AGG TGC T | 1675 |
| Val Pro Lys Arg Thr Ala Ala Val Phe Val Glu Pro Arg Cys | |
| 545 550 555 | |
| | |
| GATGGATGCC TTTCGCTAGC GAGCAAGTGC ATTCGGCATC CAAGTCGAAG CAAACGAATG | 1735 |
| AAATAAGAGA AGGCCATCGA ATAAAACGAA GTATATAAAT AGATTGAATA AGACGTTGCC | 1795 |
| CAAGTTGCCA AGGCACGCTT TGCCATATGT ATGCGTTGAA AAATAAATAA ATAAATAAAT | 1855 |
| AAATGATGTT ATAGAGGTAC AAAAGCATTG GAACATTTCT TTATAGAGGT GAACCACCCT | 1915 |
| ATTTTCCAGT TTCCATGTGT GAATTGTGAT TAGCATATGT ATGGAATAAT AATATAAATT | 1975 |
| AATTTTATGC AAAAAAAA | 1993 |

(2) INFORMATION FOR SEQ ID NO: 2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 558 amino acids
- (B) TYPE: amino acid
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 2:

| | |
|---|--|
| Gly Thr Arg Ser Lys Leu Pro Pro Gly Ser Asp Leu Gln Gln Ala Ala | |
| 1 5 10 15 | |
| Ile Val Ala Ile Gln Glu Glu Asp Pro Tyr Asn Trp Gly Tyr Asn Pro | |
| 20 25 30 | |
| Val Val Trp Gly Val Pro Lys Gly Ser Tyr Ala Ser Asn Pro Asp Gly | |
| 35 40 45 | |
| Pro Ser Arg Ile Ile Glu Tyr Arg Leu Met Val Gln Ala Leu Asn Arg | |
| 50 55 60 | |
| Leu Gly Leu Arg Val Val Met Asp Val Val Tyr Asn His Leu Tyr Ser | |
| 65 70 75 80 | |
| Ser Gly Pro Phe Ala Ile Thr Ser Val Leu Asp Lys Ile Val Pro Gly | |
| 85 90 95 | |
| Tyr Tyr Leu Arg Arg Asp Ser Asn Gly Gln Thr Glu Asn Ser Ala Ala | |
| 100 105 110 | |
| Val Asn Asn Thr Ala Ser Glu His Phe Met Val Asp Arg Leu Ile Val | |
| 115 120 125 | |
| Asp Asp Leu Leu Asn Trp Ala Val Asn Tyr Lys Val Asp Gly Phe Arg | |
| 130 135 140 | |

Phe Asp Leu Met Gly His Ile Met Lys Lys Thr Met Ile Arg Ala Lys
 145 150 155 160
 Ser Ala Leu Gln Ser Leu Thr Ile Asp Glu His Gly Val Asp Gly Ser
 165 170 175
 Lys Ile Tyr Leu Tyr Gly Glu Gly Trp Asn Phe Gly Glu Val Ala Clu
 180 185 190
 Asn Gln Arg Gly Ile Asn Gly Ser Gln Leu Asn Met Ser Gly Thr Gly
 195 200 205
 Ile Gly Ser Phe Asn Asp Arg Ile Arg Asp Ala Ile Asn Gly Gly Ser
 210 215 220
 Pro Phe Gly Asn Pro Leu Gln Gln Gly Phe Ser Thr Gly Leu Phe Leu
 225 230 235 240
 Glu Pro Asn Gly Phe Tyr Gln Gly Asn Glu Thr Glu Thr Arg Leu Thr
 245 250 255
 Leu Ala Thr Tyr Ala Asp His Ile Gln Ile Gly Leu Ala Gly Asn Leu
 260 265 270
 Lys Asp Tyr Val Val Ile Ser His Thr Gly Glu Ala Arg Lys Gly Ser
 275 280 285
 Glu Ile Arg Thr Phe Asp Gly Ser Pro Val Gly Tyr Ala Ser Ser Pro
 290 295 300
 Ile Glu Thr Ile Asn Tyr Ala Ser Ala His Asp Asn Glu Thr Leu Phe
 305 310 315 320
 Asp Ile Ile Ser Leu Lys Thr Pro Met Asp Leu Ser Ile Asp Glu Arg
 325 330 335
 Cys Arg Ile Asn His Leu Ser Thr Ser Met Ile Ala Leu Ser Gln Gly
 340 345 350
 Ile Pro Phe Phe His Ala Gly Asp Glu Ile Leu Arg Ser Lys Ser Leu
 355 360 365
 Asp Arg Asp Ser Tyr Asp Ser Gly Asp Trp Phe Asn Lys Ile Asp Phe
 370 375 380
 Thr Tyr Glu Thr Asn Asn Trp Gly Val Gly Leu Pro Pro Arg Glu Lys
 385 390 395 400
 Asn Glu Gly Ser Trp Pro Leu Met Lys Pro Arg Leu Glu Asn Pro Ser
 405 410 415
 Phe Lys Pro Ala Lys His Asp Ile Ile Ala Ala Leu Asp Lys Phe Ile
 420 425 430
 Asp Ile Leu Lys Ile Arg Tyr Ser Ser Pro Leu Phe Arg Leu Thr Thr
 435 440 445
 Ala Ser Asp Ile Val Gln Arg Val His Phe His Asn Thr Gly Pro Ser
 450 455 460

Leu Val Pro Gly Val Ile Val Met Ser Ile Glu Asp Ala Arg Asn Asp
 465 470 475 480
 Arg His Asp Met Ala Gln Ile Asp Glu Thr Phe Ser Cys Val Val Thr
 485 490 495
 Val Phe Asn Val Cys Pro Tyr Glu Val Ser Ile Glu Ile Pro Asp Leu
 500 505 510
 Ala Ser Leu Arg Leu Gln Leu His Pro Val Gln Val Asn Ser Ser Asp
 515 520 525
 Ala Leu Ala Arg Gln Ser Ala Tyr Asp Thr Ala Thr Gly Arg Phe Thr
 530 535 540
 Val Pro Lys Arg Thr Ala Ala Val Phe Val Glu Pro Arg Cys
 545 550 555

(2) INFORMATION FOR SEQ ID NO: 3:

(i) SEQUENCE DESCRIPTION:

- (A) LENGTH: 492 base pairs
- (B) TYPE: nucleotide
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA to mRNA

(iii) HYPOTHETICAL: NO

(iv) ANTISENSE: NO

(vi) ORIGINAL SOURCE:

- (A) ORGANISM: Solanum tuberosum
- (B) STRAIN: Berolina
- (F) TISSUE TYPE: tuber

(ix) FEATURE:

- (A) NAME/KEY: CDS
- (B) LAGE:1..492
- (D) OTHER INFORMATION:/product= "debranching enzyme (R-enzyme) "

(xi) SEQUENCE INFORMATION: SEQ ID NO: 3:

| | |
|---|-----|
| TCT GCT GAT GGC AAG TGG ACA TTA TTA GTT AAT CTT GAT TCT GAT GAT | 48 |
| Ser Ala Asp Gly Lys Trp Thr Leu Leu Val Asn Leu Asp Ser Asp Asp | |
| 560 565 570 | |
| GTA AAA CCT GAA GGC TGG GAT AAT CTA CAA GAC GTG AAG CCA AAT CTT | 96 |
| Val Lys Pro Glu Gly Trp Asp Asn Leu Gln Asp Val Lys Pro Asn Leu | |
| 575 580 585 590 | |
| CTT TCC TTT TCT GAT GTC AGC ATC TAT GAG CTG CAT GTT AGA GAT TTC | 144 |
| Leu Ser Phe Ser Asp Val Ser Ile Tyr Glu Leu His Val Arg Asp Phe | |
| 595 600 605 | |

| | |
|---|-----|
| ACT GCC AGT GAC CCT ACT GTG TCT CAT GAA TTT CAG GCC GGT TAT CTC Thr Ala Ser Asp Pro Thr Val Ser His Glu Phe Gln Ala Gly Tyr Leu 610 615 620 | 192 |
| GCC CCT TCC ACG TCG CAG GCA TCA GCT GGT GTC CAA CAT TTG AAA AGA Ala Pro Ser Thr Ser Gln Ala Ser Ala Gly Val Gln His Leu Lys Arg 625 630 635 | 240 |
| TTA TCA AGT GCT GGT ATC ACT CAT GTC CAC CTG TGG CCA ACC TAT CAA Leu Ser Ser Ala Gly Ile Thr His Val His Leu Trp Pro Thr Tyr Gln 640 645 650 | 288 |
| TTT GCT GGT GTC GAA GAT GAG AAA CAT AAA TGG AAG TAT ACA GAT ATC Phe Ala Gly Val Glu Asp Glu Lys His Lys Trp Lys Tyr Thr Asp Ile 655 660 665 670 | 336 |
| GAG AAA CTC AAC TCT TTT CCA CCA GAT TCT GAG GAG CAG CAG GCT CTT Glu Lys Leu Asn Ser Phe Pro Pro Asp Ser Glu Glu Gln Gln Ala Leu 675 680 685 | 384 |
| ATC ACA GCC ATC CAA GAT GAA GAT GGC TAT AAT TGG GGG TAT AAT CCT Ile Thr Ala Ile Gln Asp Glu Asp Gly Tyr Asn Trp Gly Tyr Asn Pro 690 695 700 | 432 |
| GTT CTC TGG GGA GTT CCA AAG GGA AGC TAT GCT GGT AAT GCA AAT GGT Val Leu Trp Gly Val Pro Lys Gly Ser Tyr Ala Gly Asn Ala Asn Gly 705 710 715 | 480 |
| CCT TGT CGT ATC Pro Cys Arg Ile 720 | 492 |

(2) INFORMATION FOR SEQ ID NO: 4:

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 164 amino acids
 (B) TYPE: amino acid
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO: 4:

| |
|--|
| Ser Ala Asp Gly Lys Trp Thr Leu Leu Val Asn Leu Asp Ser Asp Asp 1 5 10 15 |
| Val Lys Pro Glu Gly Trp Asp Asn Leu Gln Asp Val Lys Pro Asn Leu 20 25 30 |
| Leu Ser Phe Ser Asp Val Ser Ile Tyr Glu Leu His Val Arg Asp ine 35 40 45 |
| Thr Ala Ser Asp Pro Thr Val Ser His Glu Phe Gln Ala Gly Tyr Leu 50 55 60 |
| Ala Pro Ser Thr Ser Gln Ala Ser Ala Gly Val Gln His Leu Lys Arg 65 70 75 80 |

| | | | | | | | | | | | | | | | |
|-----------------|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|-----|
| Leu | Ser | Ser | Ala | Gly | Ile | Thr | His | Val | His | Leu | Trp | Pro | Thr | Tyr | Gln |
| | | | | 85 | | | | | 90 | | | | | 95 | |
| Phe | Ala | Gly | Val | Glu | Asp | Glu | Lys | His | Lys | Trp | Lys | Tyr | Thr | Asp | Ile |
| | | | 100 | | | | | 105 | | | | | 110 | | |
| Glu | Lys | Leu | Asn | Ser | Phe | Pro | Pro | Asp | Ser | Glu | Glu | Gln | Gln | Ala | Leu |
| | | 115 | | | | | 120 | | | | | 125 | | | |
| Ile | Thr | Ala | Ile | Gln | Asp | Glu | Asp | Gly | Tyr | Asn | Trp | Gly | Tyr | Asn | Pro |
| | 130 | | | | | 135 | | | | | 140 | | | | |
| Val | Leu | Trp | Gly | Val | Pro | Lys | Gly | Ser | Tyr | Ala | Gly | Asn | Ala | Asn | Gly |
| 145 | | | | | 150 | | | | | 155 | | | | | 160 |
| Pro Cys Arg Ile | | | | | | | | | | | | | | | |